

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: NESTEC S.A
(B) STREET: AVENUE NESTLE 55,
(C) CITY: VEVEY
(D) STATE OR PROVINCE: VAUD
(E) COUNTRY: SWITZERLAND
(F) POST CODE: 1800
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(ii) TITLE OF THE INVENTION: COFFEE MANNANASE

(iii) NUMBER OF SEQUENCES: 7

(iv) COMPUTER READABLE FORM

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1613 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TTCATTAATA	60
ATGGCCTTCT	120
CCAGGAGAAG	180
CAATATCAGC	240
AACTTCTCTT	300
GCTGCTTCCT	360
TGTGATCATC	
GTCTTATCCC	
TGCATTGCGA	
AAATCATATA	
GTTTCTTCCTT	
CTGCTTCGCG	
CTTTATTCAA	
ACAAGAGGAA	
CCCGATTCTG	
GTTAGGTGGC	
TACCCATTTC	
TTTTCAATGG	
GTTCAACTCC	
TACTGGATGA	
TGCATGTTGC	
AGCTGAGCCA	
AGTGAAAGGC	
ATAAAATTTC	
CAATGTATTT	
CGCGAGGCTG	
CTGCTACAGG	
GCTTACTGTT	
TGCCGGACAT	
GGGCATTCA	
CGATGGTGGC	
GATCGAGCTC	
TTCAAATGTC	
CCCCGGAGTC	
TATGATGAAC	
GTGTCTTC	

GGCCCTTGAT TTTGTGGTAT CGGAAGCAAG GAAGTATGGA GTTCACTTAA TCCTGAGTCT 420
 GACCAACAAAC TACAAGGACT TTGGAGGAAG GACGCAATAC GTGACGTGGG CTAAAAATGC 480
 CGGAGTACAA GTGAATAGCG ATGATGATTT TTACACCAAG AATGCTGTCA AGGGATATTA 540
 CAAGAACATCAC ATTAAGAAAG TGTTGACTAG GATCAACACA ATCACTACAG TTGCATATAA 600
 AGATGATCCA ACAGTCATGG CATGGGAGCT AATAAAATGAA CCTCGTTGCC AGGTGACTT 660
 CTCCGGAAAA ACCTTAAATG CTTGGGTTCA AGAAATGGCA ACTTACGTCA AATCACTCGA 720
 TAACAAACAC CTTCTAGAAA TAGGCATGGA GGGATTCTAC GGAGATTCAA TGCCAGGCAA 780
 AAAGCAGTAC AATCCTGGAT ACCAAGTGGG CACAGATTT ATCACCAATA ATCTTATCAA 840
 AGAGATAGAT TTTGCAACCA TTCATGCATA TCCCGATATT TGGCTGTCTG GACAGAGCGA 900
 CGGTGCACAG ATGATGTTCA TGAGAAGGTG GATGACCAGT CACTCCACAG ACTCTAAAGAC 960
 CATACTTAAA AAACCATTGG TTCTCGCTGA ATTTGGAAA TCAAGTAAAG ATCCACGGATA 1020
 CAGTTTATAT GCCAGGGAGT CATTGATGGC CGCAATTTAC GGTGATATCT ACAGGTTTGC 1080
 TAGAAGAGGA GGCATTGCAAG GTGGATTGGT TTGGCAAATC CTGGCCGAGG GAATGCAACC 1140
 GTACGCAGAT GGGTATGAAA TTGCTTGTC TCAGAACCCA TCAACCGGAC GAATCATAAG 1200
 CCAACAGTCT CGACAAATGA CTTCACTCGA CCATATGAGC AGTAATAGAA CCAATTCTCA 1260
 AAGCAACAAA CTGCGCAATT CAAAGGAGCA GTGATCAGTC TTCCAGAAAG TCTACTTGAG 1320
 TTTGTTCGTA TGTCAAAATC AAGTATCAAC CATAAGAAATT TCCATTATAT TCAGGAGTGT 1380
 TTAGTCAAGT TCTAGTAATA CCGCTGGAGT CATGATAGTT ATGACAGTAA TACCGCTGGA 1440
 GTCAAGTTCT AGTAATACCG TTGGAGTCAA GTTATGATAG TTATTTAAAA ATTAGTATTT 1500
 TATTACAAAT TTGTTATTGT TGTGAGACTT GTTATTAAAG TAAATGGAAA GTCTTATCAT 1560
 TATTATCATT TGAGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 1613

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: [lacuna]
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Phe	Ser	Arg	Arg	Ser	Asn	Ile	Ser	Asn	Phe	Ser	Cys	Cys	Phe
1															15
Leu	Val	Ile	Ile	Val	Leu	Ser	Leu	His	Cys	Glu	Asn	His	Ile	Val	Ser
20															30
Ser	Ser	Ala	Ser	Arg	Phe	Ile	Gln	Thr	Arg	Gly	Thr	Arg	Phe	Val	Leu
35															45

Gly Gly Tyr Pro Phe Phe Asn Gly Phe Asn Ser Tyr Trp Met Met
 50 55 60
 His Val Ala Ala Glu Pro Ser Glu Arg His Lys Ile Ser Asn Val Phe
 65 70 75 80
 Arg Glu Ala Ala Ala Thr Gly Leu Thr Val Cys Arg Thr Trp Ala Phe
 85 90 95
 Ser Asp Gly Gly Asp Arg Ala Leu Gln Met Ser Pro Gly Val Tyr Asp
 100 105 110
 Glu Arg Val Phe Gln Ala Leu Asp Phe Val Val Ser Glu Ala Arg Lys
 115 120 125
 Tyr Gly Val His Leu Ile Leu Ser Leu Thr Asn Asn Tyr Lys Asp Phe
 130 135 140
 Gly Gly Arg Thr Gln Tyr Val Thr Trp Ala Lys Asn Ala Gly Val Gln
 145 150 155 160
 Val Asn Ser Asp Asp Asp Phe Tyr Thr Lys Asn Ala Val Lys Gly Tyr
 165 170 175
 Tyr Lys Asn His Ile Lys Lys Val Leu Thr Arg Ile Asn Thr Ile Ser
 180 185 190
 Arg Val Ala Tyr Lys Asp Asp Pro Thr Val Met Ala Trp Glu Leu Ile
 195 200 205
 Asn Glu Pro Arg Cys Gln Val Asp Phe Ser Gly Lys Thr Leu Asn Ala
 210 215 220
 Trp Val Gln Glu Met Ala Thr Tyr Val Lys Ser Leu Asp Asn Lys His
 225 230 235 240
 Leu Leu Glu Ile Gly Met Glu Gly Phe Tyr Gly Asp Ser Met Pro Gly
 245 250 255
 Lys Lys Gln Tyr Asn Pro Gly Tyr Gln Val Gly Thr Asp Phe Ile Thr
 260 265 270
 Asn Asn Leu Ile Lys Glu Ile Asp Phe Ala Thr Ile His Ala Tyr Pro
 275 280 285
 Asp Ile Trp Leu Ser Gly Gln Ser Asp Gly Ala Gln Met Met Phe Met
 290 295 300
 Arg Arg Trp Met Thr Ser His Ser Thr Asp Ser Lys Thr Ile Leu Lys
 305 310 315 320
 Lys Pro Leu Val Leu Ala Glu Phe Gly Lys Ser Ser Lys Asp Pro Gly
 325 330 335

Tyr Ser Leu Tyr Ala Arg Glu Ser Phe Met Ala Ala Ile Tyr Gly Asp
 340 345 350
 Ile Tyr Arg Phe Ala Arg Arg Gly Gly Ile Ala Gly Gly Leu Val Trp
 355 360 365
 Gln Ile Leu Ala Glu Gly Met Gln Pro Tyr Ala Asp Gly Tyr Glu Ile
 370 375 380
 Val Leu Ser Gln Asn Pro Ser Thr Gly Arg Ile Ile Ser Gln Gln Ser
 385 390 395 400
 Arg Gln Met Thr Ser Leu Asp His Met Ser Ser Asn Arg Thr Asn Ser
 405 410 415
 Gln Ser Asn Lys Leu Arg Asn Ser Lys Glu Gln
 420 425

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGNATGGARG GNTTYTAYGG

20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTTTTTTTTT TTTTT

15

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAATCTGTGC CCACTTG

17

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGAAACAG CTATGAC

17

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: [lacuna]
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ser Phe Asn Phe Val Lys Thr Arg Gly Thr Glu Phe Val Met Asp Xaa
1 5 10 15
Arg Phe Leu Tyr Leu
20

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: [lacuna]
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Thr Trp Ala Phe Ser Asp Gly Gly Tyr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: [lacuna]
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Glu Tyr Asn Pro Gly Tyr Gln Val Gly Thr Asp Phe Ile Ser Asn Asn
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTCTTATCCC TGGATCCCGA AAATCATATA GTTTCT

36

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTACTCTGCA GACTTTCTGG AAGACTGATC ACTGCTCCCT

40